



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 154530

TO: Brian Kwon
Location: REM-3A74/3C70
Art Unit: 1614
Friday, May 27, 2005

Case Serial Number: 09/763616

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518 *BOB*

barbara.obryen@uspto.gov

Search Notes

RUSH

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11 Rush

Access DB#

154530

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Brian Kwon Examiner #: 78155 Date: 5/26/05
An Unit: 1614 Phone Number 30 _____ Serial Number: 69/262616
Mail Box and Bldg/Room Location: 3A74 Results Format Preferred (circle): PAPER DISK E-MAIL
Remson 303CM

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: therapeutic compounds and methods
Inventors (please provide full names): _____

Earliest Priority Filing Date: 7/15/99

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Sequence search for claim 32

RECEIVED

MAY 26 2005

STIC

please search commercial data base as well as
Interference Search

Thank

Rush Search
Approved

STAFF USE ONLY

Searcher: POB

Type of Search

NA Sequence (#) _____

STN _____

Vendors and cost where applicable

Searcher Phone # _____

AA Sequence (#) _____

Dialog _____

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2005, 00:22:40 ; Search time 161 Seconds
(without alignments)
88.883 Million cell updates/sec

Title: US-09-763-616-2

Perfect score: 69
Sequence: 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 segs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	100.0	37	3	Aay82461 Chelated
2	69	100.0	37	3	Aay91614 Human sec
3	69	100.0	37	8	Adl71690 Novel hum
4	69	100.0	46	3	Aag56091 Arabidops
5	69	100.0	47	8	Abos9388 Human gen
6	69	100.0	50	4	Aam13839 Peptide #
7	69	100.0	50	4	Abb32784 Peptide #
8	69	100.0	50	4	Aam26246 Peptide #
9	69	100.0	50	4	Abb27614 Human pep
10	69	100.0	50	4	Abb18267 Protein #
11	69	100.0	50	4	Aam5971 Human bon
12	69	100.0	50	4	Aam53591 Human bra
13	69	100.0	50	4	Abg47636 Human liv
14	69	100.0	50	4	Aam01583 Peptide #
15	69	100.0	50	5	Abg35618 Human pep
16	69	100.0	50	6	Aao16632 Human pap
17	69	100.0	52	3	Aay96950 Rubredoxi
18	69	100.0	53	6	Abrc63889
19	69	100.0	53	8	Adna46935 Thermococ
20	69	100.0	54	1	Aap92305 Sequence
21	69	100.0	54	8	Abos60186 Human gen
22	69	100.0	55	4	Abbs6559 Drosophil
23	69	100.0	55	6	Abbs9543 An epitop
24	69	100.0	56	4	Abbs6566 Drosophil
25	69	100.0	58	5	Abp09095 Human ORF

26	69	100.0	59	8	Adn46780 Thermococ
27	69	100.0	60	4	Aam15683 Peptide #
28	69	100.0	60	4	Aam28187 Peptide #
29	69	100.0	60	4	Abb20093 Protein #
30	69	100.0	60	4	Aam03419 Peptide #
31	69	100.0	60	5	Abg37409 Human pep
32	69	100.0	61	4	Aau39623 Propionib
33	69	100.0	61	4	Abg23599 Novel hum
34	69	100.0	61	6	Abm36142 Propionib
35	69	100.0	62	8	Adp31006 Human sec
36	69	100.0	63	4	Aam15926 Peptide #
37	69	100.0	63	4	Abbs6560 Drosophil
38	69	100.0	63	4	Abb34913 Peptide #
39	69	100.0	63	4	Aam28429 Peptide #
40	69	100.0	63	4	Abb29742 Peptide #
41	69	100.0	63	4	Abb20327 Protein #
42	69	100.0	63	4	Aam68102 Human bon
43	69	100.0	63	4	Aam55724 Human bra
44	69	100.0	63	4	Abg49752 Human liv
45	69	100.0	63	4	Aam03662 Peptide #

ALIGNMENTS

RESULT 1

AAY82461

ID AAY82461 standard; peptide; 37 AA.

AC AAY82461;

DT 30-JUN-2000 (first entry)

DE Chelated zinc domain sequence motif.

XX Chelated zinc finger; therapeutic; treatment; prophylaxis; MPV;

KW mammalian papillomavirus; antiviral; cytostatic; cervical cancer; lesion;
wart.

OS Unidentified.

FH Key Location/Qualifiers

FT Misc-difference 2 /note= "unspecified"

FT Misc-difference 3 /note= "unspecified"

FT Misc-difference 5 /note= "unspecified"

FT Misc-difference 6 /note= "unspecified"

FT Misc-difference 7 /note= "unspecified"

FT Misc-difference 8 /note= "unspecified"

FT Misc-difference 9 /note= "unspecified"

FT Misc-difference 10 /note= "unspecified"

FT Misc-difference 11 /note= "unspecified"

FT Misc-difference 12 /note= "unspecified"

FT Misc-difference 13 /note= "unspecified"

FT Misc-difference 14 /note= "unspecified"

FT Misc-difference 15 /note= "unspecified"

FT Misc-difference 16 /note= "unspecified"

FT Misc-difference 17 /note= "unspecified"

FT Misc-difference 18 /note= "unspecified"

FT Misc-difference 19 /note= "unspecified"
FT Misc-difference 20 /note= "unspecified"
FT Misc-difference 21 /note= "unspecified"
FT Misc-difference 22 /note= "unspecified"
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FT Misc-difference 24 /note= "unspecified"
FT Misc-difference 25 /note= "unspecified"
FT Misc-difference 26 /note= "unspecified"
FT Misc-difference 27 /note= "unspecified"
FT Misc-difference 28 /note= "unspecified"
FT Misc-difference 29 /note= "unspecified"
FT Misc-difference 30 /note= "unspecified"
FT Misc-difference 31 /note= "unspecified"
FT Misc-difference 32 /note= "unspecified"
FT Misc-difference 32 /note= "unspecified"
FT Misc-difference 33 /note= "unspecified"
FT Misc-difference 35 /note= "unspecified"
FT Misc-difference 36 /note= "unspecified"
FT Misc-difference 36 /note= "unspecified"
XX WO200014063-A1.
XX
XX PD 16-MAR-2000.
XX
XX PF 03-SEP-1999; 99WO-AU000724.
XX
XX PR 04-SEP-1998; 98AU-00005733.
XX PR 15-JUL-1999; 99AU-00001645.
XX
XX (MOLE-) INST MOLECULAR & CELL BIOLOGY.
XX (HUGH/) HUGHES E J L.
XX
XX PI Bernard H, Tan YJ, Beerheide W, Ting AE, Sim MM;
XX WPI; 2000-256917/22.
XX
XX The present invention describes an agent used in the treatment or prophylaxis of a disease caused or exacerbated by MPV (mammalian papillomavirus) comprising a compound capable of reducing, inhibiting or otherwise decreasing the activity of a protein encoded by an MPV gene by facilitating disruption of a chelated metal cation domain present in the protein. An agent of the present invention can be used to treat cervical cancer or its HPV associated precursor lesions or other HPV associated cancers and/or warts. The present sequence represents a specifically claimed conserved motif sequence for a chelated zinc domain
XX Sequence 37 AA;
SQ

Query Match 100.0%; Score 69; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
Db 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
RESULT 2
AAAY91614
ID AAY91614 standard; protein; 37 AA.
XX
XX AC AAY91614;
XX
XX DT 29-JUN-2000 (first entry)
XX
XX DE Human secreted protein sequence encoded by gene 17 SEQ ID NO:287.
XX
XX KW Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
KW antiHIV; antiinflammatory; neutropic; neuroprotective; antiallergic;
KW osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma;
KW antipsoriatic; cardiant; gene therapy; cancer; neurological disorder;
KW immune disease; inflammation; blood disorder; tumour.
XX
XX OS Homo sapiens.
XX
XX PN WO200006698-A1.
XX
XX PD 10-FEB-2000.
XX
XX PF 29-JUL-1999; 99WO-US017130.
XX
XX PR 30-JUL-1998; 98US-0094657P.
XX PR 05-AUG-1998; 98US-0095486P.
XX PR 06-AUG-1998; 98US-0095454P.
XX PR 06-AUG-1998; 98US-0095455P.
XX PR 12-AUG-1998; 98US-0096319P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Shi Y;
XX Lafleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer LA;
XX Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;
XX WPI; 2000-195282/17.
XX
XX New isolated human genes and the secreted polypeptides they encode,
XX useful for diagnosis and treatment of e.g. cancers, neurological
XX disorders, immune diseases, inflammation or blood disorders.
XX
XX Disclosure; Page 48; 634pp; English.
XX
XX The polynucleotide sequences given in AAA26346 to AAA26458 encode the
XX human secreted proteins given in AAY91451 to AAY91691. The human secreted
XX proteins can have activities based on the tissues and cells they are
XX expressed in. Examples of the activities are: cytostatic;
XX immunosuppressive; antiHIV; antiinflammatory; neutropic; neuroprotective;
XX antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic;
XX antiasthma; antipsoriatic; and cardiant. The polynucleotides and their
XX corresponding secreted proteins are useful for preventing, treating or
XX ameliorating medical conditions, e.g. by protein or gene therapy. Also
XX pathological conditions can be diagnosed by determining the amount of the
XX proteins in a sample or by determining the presence of mutations in the
XX polynucleotides. Specific uses are described for each of the
XX polynucleotides, based on which tissues they are most highly expressed
XX in, and include developing products for the diagnosis or treatment of
XX cancer, tumours, neurodegenerative disorders, developmental abnormalities
XX and foetal deficiencies, blood disorders, diseases of the immune system,
XX autoimmune diseases, hepatic and renal disease, inflammation, allergies,
XX Alzheimer's and behavioural disorders, schizophrenia, osteoporosis,
XX arthritis, infections, AIDS, spinal cord injuries, transplant rejection,
XX diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders,
XX

PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130049P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
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PR 06-MAY-1999; 99US-0132487P.
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PR 11-MAY-1999; 99US-01334256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
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PR 20-MAY-1999; 99US-0135124P.
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PR 21-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
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PR 08-JUN-1999; 99US-0138094P.
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PR 23-JUN-1999; 99US-0140353P.
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PR 28-JUN-1999; 99US-0140823P.
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PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
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PR 02-JUL-1999; 99US-0142154P.
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PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
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PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
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PR 20-SEP-1999; 99US-0154779P.
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PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 08-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159233P.
PR 13-OCT-1999; 99US-0159294P.

[illegible]

RESULT 11
AAM65971

RESULT 11
AAM65971

```
ID  AA065971 standard; protein; 50 AA.
XX
AC  AA065971;
XX
XX  06-NOV-2001 (first entry)
XX  Human bone marrow expressed probe encoded protein SEQ ID NO: 26277.
DE
DE  Human; bone marrow expressed exon; gene expression analysis; probe;
KW  microarray; cancer; leukaemia; lymphoma; myeloma.
XX
OS  Homo sapiens.
XX
XX  WO200157276-A2.
XX
XX  09-AUG-2001.
XX
XX  30-JAN-2001; 2001WO-US000668.
XX
XX  04-FEB-2000; 2000US-0180312P.
XX  26-MAY-2000; 2000US-0207456P.
XX  30-JUN-2000; 2000US-00608408.
XX  03-AUG-2000; 2000US-00632366.
XX  21-SEP-2000; 2000US-0234687P.
XX  27-SEP-2000; 2000US-0236359P.
XX  04-OCT-2000; 2000GB-00024263.
XX
XX  (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX  Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX  WPI; 2001-488900/53.
XX
XX  Human genome-derived single exon nucleic acid probes useful for analyzing
XX  gene expression in human bone marrow.
XX
XX  Example 4; SEQ ID NO 26277; 658pp + Sequence Listing; English.
XX
XX  The present invention provides a number of single exon nucleic acid
XX  probes which are derived from genomic sequences expressed in the human
XX  bone marrow. They can be used to measure gene expression in bone marrow
XX  samples, which may enable the improved diagnosis and treatment of cancers
XX  such as lymphoma, leukaemia and myeloma. The present sequence is a
XX  protein encoded by one of the probes of the invention
XX
XX  Sequence 50 AA;
XX
XX  Query Match 100.0%; Score 69; DB 4; Length 50;
XX  Best Local Similarity 10.8%; Pred. No. 1e+03;
XX  Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
XX  ||:||||:||||:||||:||||:||||:||||:||||:
XX  11 CIRCCGSHVQSHSLTHSRNSIRIGRLIRSECLC 47
XX
XX  RESULT 12
XX  ID  AA053591 standard; protein; 50 AA.
XX
XX  AA053591;
XX
XX  05-NOV-2001 (first entry)
XX
XX  Human brain expressed single exon probe encoded protein SEQ ID NO: 25696.
XX
XX  Human; brain expressed exon; gene expression analysis; probe; microarray;
XX  Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
XX  Homo sapiens.
XX
XX  WO200157275-A2.
XX
XX
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PD  09-AUG-2001.
XX
XX  30-JAN-2001; 2001WO-US000667.
XX
XX  04-FEB-2000; 2000US-0180312P.
XX  26-MAY-2000; 2000US-0207456P.
XX  30-JUN-2000; 2000US-00608408.
XX  03-AUG-2000; 2000US-00632366.
XX  21-SEP-2000; 2000US-0234687P.
XX  27-SEP-2000; 2000US-0236359P.
XX  04-OCT-2000; 2000GB-00024263.
XX
XX  (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX  Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX  WPI; 2001-483446/52.
XX
XX  Single exon nucleic acid probes for analyzing gene expression in human
XX  brains.
XX
XX  Example 4; SEQ ID NO 25696; 650pp + Sequence Listing; English.
XX
XX  The present invention provides a number of single exon nucleic acid
XX  probes which are derived from genomic sequences expressed in the human
XX  brain. They can be used to measure gene expression in brain cell samples,
XX  which may enable the diagnosis and improved treatment of nervous system
XX  diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX  epilepsy and cancers. The present sequence is a protein encoded by one of
XX  the probes of the invention
XX
XX  Sequence 50 AA;
XX
XX  Query Match 100.0%; Score 69; DB 4; Length 50;
XX  Best Local Similarity 10.8%; Pred. No. 1e+03;
XX  Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
XX  ||:||||:||||:||||:||||:||||:||||:||||:
XX  11 CIRCCGSHVQSHSLTHSRNSIRIGRLIRSECLC 47
XX
XX  RESULT 13
XX  ID  ABG47636 standard; peptide; 50 AA.
XX
XX  ABG47636;
XX
XX  25-FEB-2003 (first entry)
XX
XX  Human liver peptide, SEQ ID NO 26284.
XX
XX  Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX  hypercholesterolaemia; coronary heart disease.
XX
XX  Homo sapiens.
XX
XX  WO200157273-A2.
XX
XX  09-AUG-2001.
XX
XX  30-JAN-2001; 2001WO-US000664.
XX
XX  04-FEB-2000; 2000US-0180312P.
XX  26-MAY-2000; 2000US-0207456P.
XX  30-JUN-2000; 2000US-00608408.
XX  03-AUG-2000; 2000US-00632366.
XX  21-SEP-2000; 2000US-0234687P.
XX  27-SEP-2000; 2000US-0236359P.
XX  04-OCT-2000; 2000GB-00024263.
XX
XX  (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX
```

PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488898/53.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human adult liver.
 PT
 XX Claim 27; SEQ ID NO 26284; 658pp; English.
 XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
 CC measuring human gene expression in a sample derived from human adult
 CC liver, comprising one of 13109 defined nucleotide sequences given in the
 CC specification (or complements/ fragments). The probe hybridises at high
 CC stringency to a nucleic acid molecule expressed in the human adult liver.
 CC (I) may be used for predicting, measuring and displaying gene expression
 CC in samples derived from human adult liver. The genes identified may be
 CC involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
 CC associated with coronary heart disease. ABG47348-ABG59930 represent human
 CC liver single exon encoded peptides of the invention. Note: The sequence
 CC information for this patent does not appear in the printed specification
 CC but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 50 AA;
 SQ
 Query Match 100.0%; Score 69; DB 4; Length 50;
 Best Local Similarity 10.8%; Pred. No. 1e+03;
 Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 37
 DB 11 CIRCSCGVHVSRLTHSRNIRIGRLIRSECLC 47
 RESULT 14
 AA001583
 ID AA001583 standard; protein; 50 AA.
 AC AA001583;
 DT 09-OCT-2001 (first entry)
 XX Peptide #265 encoded by probe for measuring human breast gene expression.
 DE Probe; human; breast disease; breast cancer; development disorder;
 KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
 KW
 OS Homo sapiens.
 XX
 XX WO200157270-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 29-JAN-2001; 2001WO-US000661.
 XX
 XX 04-FEB-2000; 2000US-0180312P.
 XX 26-MAY-2000; 2000US-0207456P.
 XX 30-JUN-2000; 2000US-00608408.
 XX 03-AUG-2000; 2000US-00632366.
 XX 21-SEP-2000; 2000US-0234687P.
 XX 27-SEP-2000; 2000US-0236359P.
 XX 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-476286/51.
 XX Novel single exon nucleic acid probe used to measuring gene expression in
 PT a human breast.
 PT
 XX

PS Claim 27; SEQ ID NO 10323; 322pp; English.
 XX The present invention relates to novel single exon nucleic acid probes
 CC (see AAI00010-AAI10067). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for measuring human gene expression in
 CC a human breast sample, where the probe hybridises at high stringency to a
 CC nucleic acid expressed in the human breast. The probes are useful for
 CC predicting, diagnosing, grading, staging, monitoring and prognosing
 CC diseases of the human breast, particularly those diseases with polygenic
 CC aetiology. The diseases include: breast cancer, disorders of development,
 CC inflammatory diseases of the breast, fibrocystic changes, proliferative,
 CC breast disease and non-carcinoma tumours. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 50 AA;
 SQ
 Query Match 100.0%; Score 69; DB 4; Length 50;
 Best Local Similarity 10.8%; Pred. No. 1e+03;
 Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 37
 DB 11 CIRCSCGVHVSRLTHSRNIRIGRLIRSECLC 47
 RESULT 15
 ABG35618
 ID ABG35618 standard; peptide; 50 AA.
 AC ABG35618;
 XX
 XX 19-AUG-2002 (first entry)
 DT
 XX Human peptide encoded by genome-derived single exon probe SEQ ID 25283.
 DE Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200186003-A2.
 XX
 XX 15-NOV-2001.
 XX
 XX 30-JAN-2001; 2001WO-US000665.
 XX
 XX 04-FEB-2000; 2000US-0180312P.
 XX 26-MAY-2000; 2000US-0207456P.
 XX 30-JUN-2000; 2000US-00608408.
 XX 03-AUG-2000; 2000US-00632366.
 XX 21-SEP-2000; 2000US-0234687P.
 XX 27-SEP-2000; 2000US-0236359P.
 XX 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2002-114183/15.
 XX Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.
 PT
 XX Claim 27; SEQ ID NO 25283; 634pp; English.
 PS

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 00:27:20 ; Search time 42 Seconds
(without alignments)
65.762 Million cell updates/sec

Title: US-09-763-616-2

Perfect score: 69

Sequence: 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/prodata/1/iaa/5A COMB.pcp.*
- 2: /cgn2_6/prodata/1/iaa/5B COMB.pcp.*
- 3: /cgn2_6/prodata/1/iaa/6A COMB.pcp.*
- 4: /cgn2_6/prodata/1/iaa/6B COMB.pcp.*
- 5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pcp.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69	100.0	37	4	US-09-489-847-294
2	69	100.0	39	1	US-08-036-555B-40
3	69	100.0	39	1	US-08-469-569-40
4	69	100.0	39	1	US-08-249-322A-40
5	69	100.0	39	1	US-08-469-526A-40
6	69	100.0	39	2	US-08-734-591A-40
7	69	100.0	39	2	US-08-469-660-40
8	69	100.0	39	3	US-08-735-021-40
9	69	100.0	39	3	US-08-734-664A-40
10	69	100.0	39	5	PCT-US94-05083C-40
11	69	100.0	39	5	PCT-US95-06846A-40
12	69	100.0	43	3	US-09-230-196-19
13	69	100.0	45	3	US-08-900-230-46
14	69	100.0	46	2	US-08-691-814B-38
15	69	100.0	47	2	US-08-691-814B-39
16	69	100.0	47	3	US-08-482-085B-91
17	69	100.0	50	3	US-08-900-230-8
18	69	100.0	50	4	US-09-270-767-34381
19	69	100.0	50	4	US-09-270-767-49598
20	69	100.0	54	3	US-08-851-843A-183
21	69	100.0	54	3	US-08-974-549A-302
22	69	100.0	54	3	US-08-854-050-183
23	69	100.0	54	3	US-09-430-323-183
24	69	100.0	54	4	US-09-402-181B-302
25	69	100.0	54	4	US-09-721-456-302
26	69	100.0	54	6	5258287-15
27	69	100.0	54	6	5258287-15

28 69 100.0 55 3 US-08-476-509B-46 Sequence 46, Appli
29 69 100.0 55 4 US-10-125-062-4 Sequence 4, Appli
30 69 100.0 63 4 US-09-252-991A-23832 Sequence 23832, A
31 69 100.0 64 4 US-08-852-666-14 Sequence 14, Appl
32 69 100.0 66 4 US-09-471-276-941 Sequence 941, App
33 69 100.0 67 4 US-09-328-352-5686 Sequence 5686, App
34 69 100.0 77 3 US-08-061-376-11 Sequence 11, Appl
35 69 100.0 77 3 US-08-061-376-12 Sequence 12, Appl
36 69 100.0 77 4 US-09-270-767-42140 Sequence 42140, A
37 69 100.0 81 4 US-09-854-864-13 Sequence 13, Appl
38 69 100.0 88 4 US-09-270-767-33917 Sequence 33917, A
39 69 100.0 88 4 US-09-270-767-49134 Sequence 49134, A
40 69 100.0 90 4 US-09-860-793-5 Sequence 5, Appli
41 69 100.0 90 4 US-09-419-381-90 Sequence 90, Appl
42 69 100.0 97 4 US-09-690-454-211 Sequence 211, App
43 69 100.0 98 1 US-08-406-248-6 Sequence 6, Appli
44 69 100.0 98 3 US-08-075-541D-42 Sequence 42, Appl
45 69 100.0 98 3 US-09-382-616A-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-489-847-294
; Sequence 294, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 294
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-294

Query Match 100.0%; Score 69; DB 4; Length 37;
Best Local Similarity 10.8%; Pred. No. 1e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CDDCQHTGQYQCRCKPGFYRDLRRPFSAPACKPC 37

RESULT 2

US-08-036-555B-40
; Sequence 40, Application US/08036555B
; Patent No. 5530109
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Mario Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; TITLE OF INVENTION: Preparation and Use
; NUMBER OF SEQUENCES: 184

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/036,555B
; FILING DATE: 24-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 5250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 688-3884
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
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; US-08-036-555B-40
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; Query Match 100.0%; Score 69; DB 1; Length 39;
; Best Local Similarity 10.8%; Pred. No. 1.le+02;
; Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
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; Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
; Db 3 CGCKCCTTTCACRCAGAGGTCTCTCTCTCTCAGC 39
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; RESULT 3
; US-08-469-569-40
; Sequence 40, Application US/08469569
; Patent No. 5606032
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Maio Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; TITLE OF INVENTION: Preparation and Use
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,569
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 5250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 688-3884
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
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; US-08-469-569-40
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; Query Match 100.0%; Score 69; DB 1; Length 39;
; Best Local Similarity 10.8%; Pred. No. 1.le+02;
; Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
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; Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
; Db 3 CGCKCCTTTCACRCAGAGGTCTCTCTCTCTCAGC 39
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; RESULT 4
; US-08-249-322A-40
; Sequence 40, Application US/08249322A
; Patent No. 5716930
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Maio Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; TITLE OF INVENTION: Preparation and Use
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/249,322A
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 838-3884
; TELEFAX: (212) 838-9200
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-249-322A-40

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Query Match 100.0%; Score 69; DB 1; Length 39;
Best Local Similarity 10.8%; Pred. No. 1.1e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
DB 3 CGCKCCTTCACRCAAGGCTCTCTCTCTCAGC 39

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RESULT 5
US-08-469-526A-40
; Sequence 40, Application US/08469526A
; Patent No. 5792849
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew
; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael
; APPLICANT: Marchionni, Mark
; APPLICANT: Chen, Maio Su
; APPLICANT: Hiles, Ian
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; PREPARATION AND USE
; NUMBER OF SEQUENCES: 187
; CORRESPONDENCE ADDRESS:
; ADDRESS: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,526A
; FILING DATE: 06 June 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 03-JUN-1992
; APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-469-526A-40

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Query Match 100.0%; Score 69; DB 1; Length 39;
Best Local Similarity 10.8%; Pred. No. 1.1e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
DB 3 CGCKCCTTCACRCAAGGCTCTCTCTCTCAGC 39

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RESULT 6
US-08-734-591A-40
; Sequence 40, Application US/08734591A
; Patent No. 5854220
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew
; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael
; APPLICANT: Hiles, Ian
; APPLICANT: Marchionni, Mark
; APPLICANT: Chen, Mario
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; PREPARATION AND USE
; NUMBER OF SEQUENCES: 187
; CORRESPONDENCE ADDRESS:
; ADDRESS: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible Pentium
; OPERATING SYSTEM: Windows95
; SOFTWARE: WordPerfect (Version 7.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,591A
; FILING DATE: 22-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 08/470,335
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 03-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 91 07566.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 428-0200
; TELEFAX: (617) 428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-734-591A-40

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Best Local Similarity 10.8%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3 CGCKCCTTCACRCAAGGTCTCTCTCTCTCAGC 39

RESULT 7
US-08-469-660-40
; Sequence 40, Application US/08469660
; Patent No. 5876973
; GENERAL INFORMATION:
; APPLICANT: Gwynne, David I.; Marchionni, Mark;
; APPLICANT: McBurney, Robert N.
; TITLE OF INVENTION: INHIBITORS OF CELL PROLIFERATION,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; ZIP: 02111-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,660
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/011,396
; FILING DATE: 29-JAN-1993

; APPLICATION NUMBER: 07/984,085
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/951,747
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/927,337
; FILING DATE: 10-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04585/017004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: 200154
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-469-660-40

Query Match 100.0%; Score 69; DB 2; Length 39;
Best Local Similarity 10.8%; Pred. No. 1.1e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
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Db 3 CGCKCCTTCACRCAAGGTCTCTCTCTCTCAGC 39

RESULT 8
US-08-735-021-40
; Sequence 40, Application US/08735021B
; Patent No. 6194377
; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROEBANT, PAUL
; APPLICANT: MINGHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 04585/00200L
; CURRENT APPLICATION NUMBER: US/08/735,021B
; CURRENT FILING DATE: 1996-10-22
; EARLIER APPLICATION NUMBER: 08/472,065
; EARLIER FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; EARLIER APPLICATION NUMBER: 07/965,173
; EARLIER FILING DATE: 1992-10-23
; EARLIER APPLICATION NUMBER: 07/940,389
; EARLIER FILING DATE: 1992-09-03
; EARLIER APPLICATION NUMBER: 07/907,138
; EARLIER FILING DATE: 1992-06-30
; EARLIER APPLICATION NUMBER: 07/863,703
; EARLIER FILING DATE: 1992-04-03
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Bos taurus
; US-08-735-021-40

Query Match 100.0%; Score 69; DB 3; Length 39;
Best Local Similarity 10.8%; Pred. No. 1.1e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
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; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; TITLE OF INVENTION: Preparation and Use
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06846A
; FILING DATE: 25-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,322
; FILING DATE: 26-MAY-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5250.5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; PCT-US95-06846A-40

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Best Local Similarity 10.8%; Pred. No. 1.1e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
Db 3 CGCCCKCCTTACACAGAGTCTTCTCTTCTCAGC 39

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RESULT 12
US-09-230-196-19
; Sequence 19, Application US/09230196
; Patent No. 6307035
; GENERAL INFORMATION:
; APPLICANT: Rauscher III, Frank J.
; APPLICANT: Jensen, David E.
; TITLE OF INVENTION: BRCAL Associated Protein (BAP-1) and
; TITLE OF INVENTION: Uses Therefor

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; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr., PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/230,196
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/022,997
; FILING DATE: 02-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/038,109
; FILING DATE: 19-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST68BUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-230-196-19
; Query Match 100.0%; Score 69; DB 3; Length 43;
; Best Local Similarity 10.8%; Pred. No. 1.3e+02;
; Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
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;
RESULT 13
US-08-900-230-46
; Sequence 46, Application US/08900230
; Patent No. 6329197
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; TITLE OF INVENTION: DNA ENCODING GALANN GALR3 RECEPTORS AND
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of The Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/900,230
; FILING DATE: 23-JUL-1997
; CLASSIFICATION: 435

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US-08-691-814B-39				
Sequence 39,	Application US/08691814B			
Patent No. 5981218				
GENERAL INFORMATION:				
APPLICANT:	Rio, Marie-Christine			
APPLICANT:	Tomasetto, Catherine			
APPLICANT:	Basset, Paul			
APPLICANT:	Byrne, Jennifer			
TITLE OF INVENTION:	Isolated Nucleic Acid Molecules Useful			
TITLE OF INVENTION:	as Leukemia Markers and in Breast Cancer Prognosis			
NUMBER OF SEQUENCES:	124			
CORRESPONDENCE ADDRESS:				
ADDRESSEE:	Sterne, Kessler, Goldstein & Fox P.L.L.C.			
STREET:	1100 New York Ave, NW, Suite 600			
CITY:	Washington			
STATE:	DC			
COUNTRY:	USA			
ZIP:	20005-3934			
COMPUTER READABLE FORM:				
MEDIUM TYPE:	Floppy disk			
COMPUTER:	IBM PC compatible			
OPERATING SYSTEM:	PC-DOS/MS-DOS			
SOFTWARE:	PatentIn Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:				
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FILING DATE:	31-JUL-1996			
CLASSIFICATION:	435			
PRIOR APPLICATION DATA:				
APPLICATION NUMBER:	US 60/002,183			
FILING DATE:	09-AUG-1995			
ATTORNEY/AGENT INFORMATION:				
NAME:	Steffe, Eric K.			
REGISTRATION NUMBER:	36,688			
REFERENCE/DOCKET NUMBER:	1383.0090001			
TELEPHONE:	202-371-2600			
TELEFAX:	202-371-2543			
INFORMATION FOR SEQ ID NO:	39:			
SEQUENCE CHARACTERISTICS:				
LENGTH:	47 amino acids			
TYPE:	amino acid			
STRANDEDNESS:	not relevant			
TOPOLOGY:	not relevant			
MOLECULE TYPE:	peptide			
US-08-691-814B-39				
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Best Local Similarity	10.8%;	Pred. No. 1.5e+02;		
Matches	4;	Conservative 33;	Mismatches 0;	Indels 0;
Gaps				
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Search completed:	May 27, 2005,	00:36:54		
Job time:	43 secs			

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 00:35:31 ; Search time 138 Seconds
(without alignments)
92.493 Million cell updates/sec

Title: US-09-763-616-2

Perfect score: 69

Sequence: 1 CXKXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37

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Searched: 1462099 seqs, 344972447 residues

Total number of hits satisfying chosen parameters: 1462099

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69	100.0	37	15 US-10-351-334-294	Sequence 294, App
2	69	100.0	39	8 US-08-736-019-40	Sequence 40, Appl
3	69	100.0	39	17 US-10-844-218-40	Sequence 40, Appl
4	69	100.0	45	8 US-08-900-230-46	Sequence 46, Appl
5	69	100.0	47	14 US-10-029-386-33022	Sequence 33022, A
6	69	100.0	50	8 US-08-900-230-8	Sequence 8, Appl
7	69	100.0	50	9 US-09-864-761-33565	Sequence 33565, A
8	69	100.0	50	17 US-10-864-774-8	Sequence 8, Appl
9	69	100.0	53	15 US-10-347-542-31	Sequence 31, Appl
10	69	100.0	54	9 US-09-843-676-183	Sequence 183, App
11	69	100.0	54	10 US-09-438-486-183	Sequence 183, App
12	69	100.0	54	14 US-10-053-758-183	Sequence 183, App
13	69	100.0	54	14 US-10-054-295-183	Sequence 183, App

14	69	100.0	54	14	US-10-054-611-183	Sequence 183, App
15	69	100.0	54	14	US-10-029-386-33820	Sequence 33820, A
16	69	100.0	54	15	US-10-325-810-302	Sequence 302, App
17	69	100.0	54	17	US-10-877-146-302	Sequence 302, App
18	69	100.0	55	13	US-10-125-062-4	Sequence 4, Appl
19	69	100.0	55	17	US-10-900-857-4	Sequence 4, Appl
20	69	100.0	57	15	US-10-424-599-198399	Sequence 198399, A
21	69	100.0	60	9	US-09-864-761-35391	Sequence 35391, A
22	69	100.0	60	15	US-10-424-599-191604	Sequence 191604, A
23	69	100.0	63	9	US-09-864-761-35525	Sequence 35525, A
24	69	100.0	66	15	US-10-424-599-129902	Sequence 129902, A
25	69	100.0	66	15	US-10-424-599-246606	Sequence 246606, A
26	69	100.0	66	17	US-10-926-683-941	Sequence 941, App
27	69	100.0	67	15	US-10-424-599-188842	Sequence 188842, A
28	69	100.0	68	15	US-10-424-599-195690	Sequence 195690, A
29	69	100.0	68	15	US-10-424-599-245913	Sequence 245913, A
30	69	100.0	68	16	US-10-437-963-129827	Sequence 129827, A
31	69	100.0	69	15	US-10-424-599-251423	Sequence 251423, A
32	69	100.0	70	15	US-10-347-542-32	Sequence 32, Appl
33	69	100.0	70	15	US-10-424-599-202673	Sequence 202673, A
34	69	100.0	71	9	US-09-864-761-42524	Sequence 42524, A
35	69	100.0	71	14	US-10-011-931-14	Sequence 14, Appl
36	69	100.0	71	14	US-10-011-931-15	Sequence 15, Appl
37	69	100.0	71	14	US-10-011-931-30	Sequence 30, Appl
38	69	100.0	71	14	US-10-011-931-31	Sequence 31, Appl
39	69	100.0	71	14	US-10-011-931-32	Sequence 32, Appl
40	69	100.0	71	14	US-10-011-931-33	Sequence 33, Appl
41	69	100.0	71	14	US-10-269-806-114	Sequence 114, App
42	69	100.0	71	16	US-10-767-701-33777	Sequence 33777, A
43	69	100.0	71	17	US-10-985-299-14	Sequence 14, Appl
44	69	100.0	71	17	US-10-985-299-15	Sequence 15, Appl
45	69	100.0	71	17	US-10-985-299-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1

US-10-351-334-294

Sequence 294, Application US/10351334

Publication No. US20040034196A1

GENERAL INFORMATION:

APPLICANT: Komatsoulis et al

TITLE OF INVENTION: 98 Human Secreted Proteins

FILE REFERENCE: P2031P2

CURRENT APPLICATION NUMBER: US/10/351,334

CURRENT FILING DATE: 2003-01-27

PRIOR APPLICATION NUMBER: 60/350,898

PRIOR FILING DATE: 2002-01-25

PRIOR APPLICATION NUMBER: 09/489,847

PRIOR FILING DATE: 2000-01-24

PRIOR APPLICATION NUMBER: PCT/US99/17130

PRIOR FILING DATE: 1999-07-29

PRIOR APPLICATION NUMBER: 60/094,657

PRIOR FILING DATE: 1998-07-30

PRIOR APPLICATION NUMBER: 60/095,486

PRIOR FILING DATE: 1998-08-05

PRIOR APPLICATION NUMBER: 60/096,319

PRIOR FILING DATE: 1998-08-12

PRIOR APPLICATION NUMBER: 60/095,454

PRIOR FILING DATE: 1998-08-06

PRIOR APPLICATION NUMBER: 60/095,455

PRIOR FILING DATE: 1998-08-06

NUMBER OF SEQ ID NOS: 376

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 294

LENGTH: 37

TYPE: PRT

ORGANISM: Homo sapiens

US-10-351-334-294

Query Match 100.0%; Score 69; DB 15; Length 37;
Best Local Similarity 10.8%; Pred. No. 5.8e+02;

Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 69; DB 8; Length 39;
 Best Local Similarity 10.8%; Pred. No. 6.2e+02;
 Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
 US-08-736-019-40
 ; Sequence 40, Application US/08736019
 ; Publication No. US20030207799A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goodearl, Andrew
 ; APPLICANT: Stroobant, Paul
 ; APPLICANT: Minghetti, Luisa
 ; APPLICANT: Waterfield, Michael
 ; APPLICANT: Marchionni, Mark
 ; APPLICANT: Chen, Mario
 ; APPLICANT: Hiles, Ian
 ; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
 ; TITLE OF INVENTION: PREPARATION AND USE
 ; NUMBER OF SEQUENCES: 189
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Clark & Elbing LLP
 ; STREET: 176 Federal Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; COMPUTER: IBM Compatible Pentium
 ; OPERATING SYSTEM: Windows95
 ; SOFTWARE: FastSeq Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/736,019
 ; FILING DATE: 22-OCT-1996
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/471,833
 ; FILING DATE: 06-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/036,555
 ; FILING DATE: 24-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/965,173
 ; FILING DATE: 23-OCT-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/907,138
 ; FILING DATE: 30-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/940,389
 ; FILING DATE: 03-SEP-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/863,703
 ; FILING DATE: 03-APR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: UK 91 07566.3
 ; FILING DATE: 10-APR-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bieker-Brady, Kristina
 ; REGISTRATION NUMBER: 39,109
 ; REFERENCE/DOCKET NUMBER: 04585/00200Q
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 428-0200
 ; TELEFAX: (617) 428-7045
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 40:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 39
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear

Query Match 100.0%; Score 69; DB 17; Length 39;
 Best Local Similarity 10.8%; Pred. No. 6.2e+02;
 Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 CDDCQHTGQYQCRKPGFYDLRRPFSAPDACKPC 37

RESULT 3
 US-10-844-218-40
 ; Sequence 40, Application US/10844218
 ; Publication No. US20050106666A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
 ; Chen, Mario Su; Hiles, Ian
 ; TITLE OF INVENTION: Glial Mitogenic Factors, Their
 ; TITLE OF INVENTION: Preparation and Use
 ; NUMBER OF SEQUENCES: 184
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pelfe & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York City
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 ; COMPUTER: IBM
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: Wordperfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/844,218
 ; FILING DATE: 12-AUG-2004
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/036,555
 ; FILING DATE: 24-MAR-1993
 ; APPLICATION NUMBER: 07/965,173
 ; FILING DATE: 23-OCT-1992
 ; APPLICATION NUMBER: 07/940,389
 ; FILING DATE: 03-SEP-1992
 ; APPLICATION NUMBER: 07/907,138
 ; FILING DATE: 30-JUN-1992
 ; APPLICATION NUMBER: 07/863,703
 ; FILING DATE: 03-APRIL-1992
 ; APPLICATION NUMBER: U.K. 91 07566.3
 ; FILING DATE: 10-APRIL-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Tsai, Christine H.
 ; REGISTRATION NUMBER: 34,266
 ; REFERENCE/DOCKET NUMBER: LUD 5250.4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 688-9200
 ; TELEFAX: (212) 838-3884
 ; INFORMATION FOR SEQ ID NO: 40:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 39
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
 US-10-844-218-40

Query Match 100.0%; Score 69; DB 17; Length 39;
 Best Local Similarity 10.8%; Pred. No. 6.2e+02;
 Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 CDDCQHTGQYQCRKPGFYDLRRPFSAPDACKPC 37


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; Sequence 33565, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33565
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000091.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 7.5
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 9.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 15
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 11
; OTHER INFORMATION: EST HUMAN HIT: A1890146.1, EVALUATE 3.40e+00
; OTHER INFORMATION: SWISSPROT HIT: Q61282, EVALUATE 6.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: AA932293.1, EVALUATE 5.10e+00
; US-09-864-761-33565
; Query Match 100.0%; Score 69; DB 9; Length 50;
; Best Local Similarity 10.8%; Pred. No. 8.6e+02;
; Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

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Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXC 37
DB 11 CIRCCGSHVQSHSLTHSRNSIRIGRLIRSECLC 47
RESULT 8
US-10-864-774-8
; Sequence 8, Application US/10864774
; Publication No. US20050090646A1
; GENERAL INFORMATION:
; APPLICANT: SULLIVAN, SEAN M.
; TITLE OF INVENTION: GENE DELIVERY TO TUMORS
; FILE REFERENCE: 5853-337-1W0
; CURRENT APPLICATION NUMBER: US/10/864,774
; CURRENT FILING DATE: 2004-06-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-10-864-774-8
; Query Match 100.0%; Score 69; DB 17; Length 50;
; Best Local Similarity 10.8%; Pred. No. 8.6e+02;
; Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXC 37
DB 9 CTTCACTATTTTCATTCCTCAATGGGTGACTTTGCTTC 45
RESULT 9
US-10-347-542-31
; Sequence 31, Application US/10347542
; Publication No. US20040009530A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, David
; APPLICANT: No. US20040009530alk, Steffen
; APPLICANT: Wagstrom, Christopher
; APPLICANT: Wu, Jiangchun
; APPLICANT: Uemura, Robyn
; TITLE OF INVENTION: ENGINEERED BINDING PROTEINS
; FILE REFERENCE: 11001-006-999
; CURRENT APPLICATION NUMBER: US/10/347,542
; CURRENT FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Pyrococcus furiosus
; US-10-347-542-31
; Query Match 100.0%; Score 69; DB 15; Length 53;
; Best Local Similarity 10.8%; Pred. No. 9.3e+02;
; Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXC 37
DB 5 CKICGYIDEDAGDPDNGISPGTKFELPDDWVCPIC 41
RESULT 10
US-09-843-676-183
; Sequence 183, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru

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; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 183:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 183:
US-10-054-611-183

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Query Match      100.0%; Score 69; DB 14; Length 54;
Best Local Similarity 10.8%; Pred. No. 9.5e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 37
Db 3 CSACSTTSGRGAPASWAPLCWMTSTGPGAPSCCV 39

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RESULT 15

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US-10-029-386-33820
; Sequence 33820, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: EXPRESSION ANALYSIS TWO
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33820
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC002455.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
; OTHER INFORMATION: SWISSPROT HIT: P34088, EVALUE 1.60e+00
US-10-029-386-33820

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Query Match      100.0%; Score 69; DB 14; Length 54;
Best Local Similarity 10.8%; Pred. No. 9.5e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 37
Db 3 CPQCWRAQSGHRCMCNTVWPRHSVWLMLLVTICRCC 39

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Search completed: May 27, 2005, 00:48:47
Job time : 149 secs

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GenCore version 5.1.6
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OM protein.- protein search, using sw model

Run on: May 27, 2005, 00:26:25 ; Search time 39 Seconds
(without alignments)
91.283 Million cell updates/sec

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Title: US-09-763-616-2
Perfect score: 69
Sequence: 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXXC 37

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Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

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1:  _pir1:*
2:  pir2:*
3:  pir3:*
4:  pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	69	100.0	52	1	A3173	rubredoxin [valida
2	69	100.0	52	1	JX0241	rubredoxin - Desul
3	69	100.0	52	1	RUDV	rubredoxin [valida
4	69	100.0	52	1	RUDVEG	rubredoxin [valida
5	69	100.0	52	2	S65620	rubredoxin - Helio
6	69	100.0	52	2	G71256	probable rubredoxi
7	69	100.0	53	1	A27537	rubredoxin - Chlor
8	69	100.0	53	1	A33182	rubredoxin - Clost
9	69	100.0	53	1	H00127	rubredoxin - "Buty
10	69	100.0	53	2	H69359	rubredoxin (rd-1)
11	69	100.0	53	2	H72348	rubredoxin - Therm
12	69	100.0	53	2	B69075	rubredoxin - Metha
13	69	100.0	53	2	E75136	rubredoxin - PA87224
14	69	100.0	54	1	JU0074	rubredoxin - Clost
15	69	100.0	54	1	RUCLEP	rubredoxin [valida
16	69	100.0	54	1	RUPF	rubredoxin [valida
17	69	100.0	54	2	G97241	rubredoxin [import
18	69	100.0	54	2	I39520	rubredoxin - Acine
19	69	100.0	54	2	AE2375	rubredoxin [import
20	69	100.0	55	2	E70593	probable ruba prot
21	69	100.0	55	2	H82976	rubredoxin PA5350
22	69	100.0	55	2	A82977	rubredoxin PA5351
23	69	100.0	55	2	S25774	testis-specific pr
24	69	100.0	56	1	WTFE	testis-specific pr
25	69	100.0	56	2	H81133	rubredoxin NMB0393
26	69	100.0	56	2	F69517	ferredoxin (fdx-8)
27	69	100.0	57	2	B82814	rubredoxin XF0379
28	69	100.0	58	2	E97333	ferredoxin [import
29	69	100.0	58	2	B42960	ferredoxin 2[4Fe-4

ALIGNMENTS

RESULT 1

A33173
rubredoxin [validated] - Clostridium thermosaccharolyticum
C;Species: Clostridium thermosaccharolyticum, Clostridium tartarivorum
C;Date: 30-Apr-1991 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: A33173
R;Meyer, J.; Gagnon, J.; Sieker, L.C.; Van Dorsselaer, A.; Moulis, J.M.
Biochem. J. 271, 839-841, 1990
A;Title: Rubredoxin from Clostridium thermosaccharolyticum. Amino acid sequ
A;Reference number: A33173; MUID:91058526; PMID:2244894

Query Match 100.0%; Score 69; DB 1; Length 52;
Best Local Similarity 10.8%; Pred. No. 3.1e+02;

[illegible]

RESULT 2

JX0241
 rubredoxin - Desulfovibrio vulgaris (strain Miyazaki)
 C:Species: Desulfovibrio vulgaris
 C:date: 10-Jun-1993 #sequence_revision 22-Jul-1994 #text_change 09-Jul-2004
 C:accession: JX0241
 R:Shimizu, F.; Ogata, M.; Yagi, T.; Wakabayashi, S.; Matsuura, H.
 Biochimie 71, 1171-1177, 1989
 A>Title: Amino acid sequence and function of rubredoxin from Desulfovibrio
 A:Reference number: JX0241: MUID:90234754: PMID:25611345

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Query Match      100.0%; Score 69; DB 1; Length 52;
Best Local Similarity 10.8%; Pred. No. 3.1e+02;
Matches 4; Conservative 33; Mismatches 0; Indels
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submitted to the Brookhaven Protein Data Bank, March 1988

A;Reference number: A50332; PDB:1RDXG
A;Contents: annotation; X-ray crystallography, 1.4 angstroms, residues 1-52
R;Prev. M.; Sieker, L.; Pavan, F.; Haser, R.; Bruschi, M.; Pepe, G.; LeGall, J.
J. Mol. Biol. 197, 525-541, 1987
A;Title: Rubredoxin from Desulfovibrio gigas. A molecular model of the oxidized form at
F;Modified site: N-formylmethionine #status experimental
F;6,9,39,42/Binding site: iron (Cys)

Query Match 100.0%; Score 69; DB 1; Length 52;
Best Local Similarity 10.8%; Pred. No. 3.1e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXKXXXXXXXXXXXXXXXKXXXXXXXXXXXXXKCXC 37
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Db 6 CTVCGYEYPAGKDPSGIKGTKFDLPDDWACPVC 42

RESULT 5

S65620
rubredoxin - Helicobacillus mobilis
C;Species: Helicobacillus mobilis
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S65620
R;Lee, W.Y.; Brune, D.C.; LoBrutto, R.; Blankenship, R.E.
Arch. Biochem. Biophys. 318, 80-88, 1995
A;Title: Isolation, characterization, and primary structure of rubredoxin from the phot
A;Reference number: S65620; PMID:95243660; PMID:7726577
A;Accession: S65620
A;Molecule type: protein
A;Cross-references: UNIPROT:P56263
C;Comment: Rubredoxin is a nonheme iron protein and substitutes for ferredoxin in some
C;Superfamily: rubredoxin; rubredoxin homology
C;Keywords: electron transfer; hydrocarbon hydroxylation; iron; metalloprotein
F;3-49/Domain: rubredoxin homology <RUB>
F;1/Modified site: N-formylmethionine #status experimental
F;6,9,39,42/Binding site: iron (Cys) #status predicted

Query Match 100.0%; Score 69; DB 2; Length 52;
Best Local Similarity 10.8%; Pred. No. 3.1e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXKXXXXXXXXXXXXXXXKXXXXXXXXXXXXXKCXC 37
 |::|:||||:||||:||||:||||:||||:||||:||
Db 6 CLVCGYYVDPAKGDPDHGIAPGTAFEDLPADWVCPCLC 42

RESULT 6

G71256
probable rubredoxin - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: G71256
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gw
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McI
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; PMID:9832770; PMID:19665876
A;Accession: G71256
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-52 <COL>
A;Cross-references: UNIPROT:O83956; GB:AEO01266; GB:AEO00520; NTID:g3323309; PIDN:AAC65!
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0991

Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and bacteria
A;Reference number: A72200; PMID:103605

Search completed: May 27, 2005, 00:36:06
Job time : 40 secs

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Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	69	100.0	51	1	ZNFP_LYCV	P19326	lymphocytic
2	69	100.0	51	2	R8P5R8	Q8P5R8	xanthomonas
3	69	100.0	51	2	Q8PH46	Q8PH46	xanthomonas
4	69	100.0	52	1	RUB2_CHL	P59993	chlorobium
5	69	100.0	52	1	RUB2_CLO	P19500	clostridium
6	69	100.0	52	1	RUBR_DS	P00270	desulfovibrio
7	69	100.0	52	1	RUBR_DS	P00269	desulfovibrio
8	69	100.0	52	1	RUBR_DS	P15412	desulfovibrio
9	69	100.0	52	1	RUBR_H	P52663	heliobacillus
10	69	100.0	52	1	RUBR_T	O83956	treponema
11	69	100.0	52	2	Q6QA00	Q6QA00	droso
12	69	100.0	52	2	Q9X709	Q9X709	clostridium
13	69	100.0	52	2	Q8R870	O8-870	thermoanaerobacter
14	69	100.0	52	2	Q73NV0	O73NV0	treponema
15	69	100.0	52	2	Q747S7	O747S7	geobacter
16	69	100.0	52	2	Q74EW2	O74EW2	geobacter
17	69	100.0	53	1	RUB1_C	Q8XMB2	clostridium
18	69	100.0	53	1	RUB2_C	P14072	clostridium
19	69	100.0	53	1	RUB3_C	P58025	chlorobium
20	69	100.0	53	1	RUBR_B	P14071	butyrivibrio
21	69	100.0	53	1	RUBR_C	P09947	chlorobium
22	69	100.0	53	1	RUBR_C	P23474	clostridium
23	69	100.0	53	1	RUBR_P	Q9V099	pyrococcus
24	69	100.0	53	1	RUBR_P	P24297	pyrococcus
25	69	100.0	53	2	O26259	O26259	methanobacter
26	69	100.0	53	2	O29381	O29381	archaeoglobus
27	69	100.0	53	2	P96745	P96745	clostridium
28	69	100.0	53	2	Q46496	Q46496	desulfococcus
29	69	100.0	53	2	Q9FDN9	Q9FDN9	moorella
30	69	100.0	53	2	Q64N49	Q64N49	bacteroides
31	69	100.0	53	2	Q9WZC7	Q9WZC7	thermotoga

RN [1] —

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RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities";
RL Nature 417:459-463(2002).
DR HSP; P00268; IIRO.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR004039; Rubredox.
DR Pfam; PF00301; Rubredoxin; 1.
DR ProDom; PD001610; Rubredox; 1.
DR PROSITE; PS00202; RUBREDOXIN; UNKNOWN 1.
DR PROSITE; PS0903; RUBREDOXIN_LIKE; 1.
DR Complete proteome.
KW Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
SQ SEQUENCE 51 AA; 5679 MW; 7A25C67893030E8F CRC64;

Query Match 100.0%; Score 69; DB 2; Length 51;
Best Local Similarity 10.8%; Pred. No. 5.1e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
Db 2 CVVCGFLYHEADGIPGEGAPGTWQDVPDWTCPDC 38

RESULT 3
Q8PH46 PRELIMINARY; PRT; 51 AA.
AC Q8PH46;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Rubredoxin.
GN Name=ruba; OrderedLocusNames=YAC3414;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities";
RL Nature 417:459-463(2002).
DR HSP; P00270; IRDQ.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR004039; Rubredox.
DR Pfam; PF00301; Rubredoxin; 1.
DR ProDom; PD001610; Rubredox; 1.
DR PROSITE; PS00202; RUBREDOXIN; UNKNOWN 1.
DR PROSITE; PS0903; RUBREDOXIN_LIKE; 1.
DR Complete proteome.
KW Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
SQ SEQUENCE 51 AA; 5679 MW; 7A25C67893030E8F CRC64;

Query Match 100.0%; Score 69; DB 2; Length 51;
Best Local Similarity 10.8%; Pred. No. 5.1e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
Db 2 CVVCGFLYHEADGIPGEGAPGTWQDVPDWTCPDC 38

RESULT 4
RUB2 CHLTE STANDARD; PRT; 52 AA.
ID RUB2 CHLTE STANDARD; PRT; 52 AA.
AC P58993;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Rubredoxin 2 (Rd 2).
GN Name=rub2; Synonym=rbr-2; OrderedLocusNames=CTII101;
OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobaculum.
OX NCBI_TaxID=1097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TLS / ATCC 49652 / DSM 12025;
RX MEDLINE=22103685; PubMed=12093901; DOI=10.1073/pnas.132181499;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson R.J., DeBoy R.T., Gwinn M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.F., Yang F.,
RA Holt I.E., Umayam L.A., Mason T.M., Brenner M., Shea T.P.,
RA Parksey D.S., Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B.,
RA Radune D., Vamathevan J.J., Khouri H.M., White O., Gruber T.M.,
RA Ketchum K.A., Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RA "The complete genome sequence of Chlorobium tepidum TLS, a
RA photosynthetic, anaerobic, green-sulfur bacterium.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
CC -!- FUNCTION: Serves as an electron acceptor for pyruvate ferredoxin
CC oxidoreductase (PFOR) (By similarity).
CC -!- COFACTOR: Binds 1 iron(III) ion per subunit (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the rubredoxin family.
CC -!- SIMILARITY: Contains 1 rubredoxin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; AE012873; AAM72334.1; -.
CC HSP; P24297; 1BQ8.
CC TIGR; CTII01; -.
CC InterPro; IPR004039; Rubredox.

```


Db 6 CTVCGYDPAEGDPDNGVKPGTSFDDLPADWVCPC 42

Formylation; Iron; Metal-binding; Rubredoxin.

MOD RES 1 1 N-formylmethionine.
FT DOMAIN 1 52 Rubredoxin-like.
FT METAL 6 6 Iron.
FT METAL 9 9 Iron.
FT METAL 39 39 Iron.
FT METAL 42 42 Iron.
FT STRAND 4 6
FT TURN 7 9
FT STRAND 12 13
FT TURN 15 17
FT STRAND 19 19
FT HELIX 20 22
FT TURN 23 23
FT STRAND 24 24
FT TURN 26 27
FT HELIX 30 32
FT TURN 35 36
FT STRAND 38 38
FT TURN 40 42
FT STRAND 45 45
FT HELIX 46 48
FT STRAND 49 52
SQ SEQUENCE 52 AA; 5598 MW; 6443741AB8A8063A2 CRC64;

RESULT 8

RUBR_DESVM

ID RUBR_DESVM STANDARD; PRT; 52 AA.

AC P15412;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Rubredoxin (Rd).

GN Name-rub;

OS Desulfovibrio vulgaris (strain Miyazaki).

OC Bacteria; Proteobacteria; Deitaproteobacteria; Desulfovibrionales;

OC Desulfovibrionaceae; Desulfovibrio.

OX NCBI_TaxID=883;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Isolate F;

RX MEDLINE=97236449; PubMed=9116039; DOI=10.1016/S0167-4781(96)00203-5;

RA Kitamura M., Koshino Y., Kamikawa Y., Kohno K., Kojima S., Miura K.,

RA Sagata T., Akutsu H., Kumagai I., Nakaya T.;

RT "Cloning and expression of the rubredoxin gene from Desulfovibrio

RT vulgaris (Miyazaki F) -- comparison of the primary structure of

RT desulfoferrodoxin.";

RL Biochim. Biophys. Acta 1351:239-247(1997).

RN [2]

RP SEQUENCE.

RX MEDLINE=90234754; PubMed=2561345; DOI=10.1016/0300-9084(89)90020-5;

RA Shimizu F., Ogata M., Yagi T., Wakabayashi S., Matsubara H.;

RA "Amino acid sequence and function of rubredoxin from Desulfovibrio

RT vulgaris Miyazaki.";

RL Biochimie 71:1171-1177(1989).

RN [3]

RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

RC STRAIN=IAM 12604;

RX MEDLINE=99190893; PubMed=10089348; DOI=10.1107/S0907444998011810;

RA Misaki S., Morimoto Y., Ogata M., Yagi T., Higuchi Y., Yasuoka N.;

RT "Structure determination of rubredoxin from Desulfovibrio vulgaris

RT Miyazaki F in two crystal forms";

RL Acta Crystallogr. D 55:408-413(1999).

CC -1- FUNCTION: Rubredoxin is a small nonheme, iron protein lacking

CC acid-labile sulfide. Its single Fe, chelated to 4 Cys, functions

CC as an electron acceptor and may also stabilize the conformation of

CC the molecule.

CC -1- FUNCTION: Electron acceptor for cytoplasmic lactate dehydrogenase.

CC -1- COFACTOR: Binds 1 iron(III) ion per subunit.

CC -1- SUBUNIT: Monomer.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: Belongs to the rubredoxin family.

CC -1- SIMILARITY: Contains 1 rubredoxin-like domain.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; D76419; BAA11175.1; -

DR PIR; JX0241; JX0241.

DR PDB; 1RDV; X-ray; @=1-52.

DR PDB; 2RDV; X-ray; A/B/C=1-52.

DR InterPro; IPR004039; Rubredox.

DR InterPro; IPR001052; Rubredoxin.

DR Pfam; PF00301; Rubredoxin; 1.

DR PRINTS; PR00163; RUBREDOXIN.

DR ProDom; PD001610; Rubredox; 1.

DR PROSITE; PS00202; RUBREDOXIN, 1.

DR PROSITE; PS00903; RUBREDOXIN LIKE, 1.

KW 3D-structure; Direct protein sequencing; Electron transport;

Query Match 100.0%; Score 69; DB 1; Length 52;

Best Local Similarity 10.8%; Pred. No. 5.2e+02;

Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXXC 37

DB 6 CTVCGYDPAEGDPDNGVKPGTSFDDLPADWVCPC 42

RESULT 9

RUBR_HELMO

ID RUBR_HELMO STANDARD; PRT; 52 AA.

AC P56263;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Rubredoxin (Rd).

OS Helicobacillus mobilis.

OC Bacteria; Firmicutes; Clostridia; Clostridiales; Helicobacteriaceae;

OC Helicobacillus.

OX NCBI_TaxID=28064;

RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.

RX MEDLINE=95243660; PubMed=7726577; DOI=10.1006/abbi.1995.1207;

RA Lee W.Y., Brune D.C., Lohrutto R., Blankenship R.E.;

RT "Isolation, characterization, and primary structure of rubredoxin from

RT the photosynthetic bacterium, Helicobacillus mobilis.";

RL Arch. Biochem. Biophys. 318:80-88(1995).

CC -1- FUNCTION: Rubredoxin is a small nonheme, iron protein lacking

CC acid-labile sulfide. Its single Fe, chelated to 4 Cys, functions

CC as an electron acceptor and may also stabilize the conformation of

CC the molecule.

CC -1- COFACTOR: Binds 1 iron(III) ion per subunit (By similarity).

CC -1- MASS SPECTROMETRY: MW=5671.3; METHOD=MALDI; RANGE=1-52;

CC NOTE=Ref.1.

CC -1- SIMILARITY: Belongs to the rubredoxin family.

CC -1- SIMILARITY: Contains 1 rubredoxin-like domain.

DR PIR; S65620; S65620.

DR HSSP; P15412; 2RDV.

DR InterPro; IPR004039; Rubredox.

DR InterPro; IPR001052; Rubredoxin.

DR Pfam; PF00301; Rubredoxin; 1.

DR PRINTS; PR00163; RUBREDOXIN.

DR ProDom; PD001610; Rubredox; 1.

DR PROSITE; PS00202; RUBREDOXIN, 1.

DR PROSITE; PS00903; RUBREDOXIN LIKE, 1.

KW Direct protein sequencing; Electron transport; Formylation; Iron;

KW Metal-binding; Rubredoxin.

```

FT MOD_RES 1 1 N-formylmethionine.
FT DOMAIN 1 52 Rubredoxin-like.
FT METAL 6 6 Iron (By similarity).
FT METAL 9 9 Iron (By similarity).
FT METAL 39 39 Iron (By similarity).
FT METAL 42 42 Iron (By similarity).
SQ SEQUENCE 52 AA; 5619 MW; 65924113D3124AD CRC64;

Query Match 100.0%; Score 69; DB 1; Length 52;
Best Local Similarity 10.8%; Pred. No. 5.2e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXCXKXXXXXXXXXXXXXXXXXXXXXKXC 37
Db 6 CLVGVYDDPAKGDPDHGIAPTGFADLPADWVCPIC 42

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RESULT	ID	RUBR_TREPA	STANDARD;	PRT;	52 AA.
	AC	083956;			
	DT	15-DEC-1998 (Rel. 37, Created)			
	DT	15-DEC-1998 (Rel. 37, Last sequence update)			
	DT	25-OCT-2004 (Rel. 45, Last annotation update)			
	DE	Rubredoxin (Rd)			
	GN	OrderedLocusNames=TP0991;			
	OS	Treponema pallidum.			
	OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.			
	OX	NCBI_TaxID=160;			
	RN	[1]			
	RP	SEQUENCE FROM N.A.			

RX MEDLINE=98332770; PubMed=9665876; DOI=10.1126/science.281.5375.375;
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
 RA Dodson R.J., Gwinn M.L., Hickey E.K., Clayton R.A., Ketchum K.A.,
 RA Soergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.D.,
 RA Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M.,
 RA Uutterback T.R., McDonald L.A., Artach P., Bowman C., Cotton M.D.,
 RA Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M.,
 RA Weidman J.F., Smith H.O., Venter J.C.;
 RT "Complete genome sequence of *Treponema pallidum*, the syphilis
 RT spirochete";
 RL Science 281:375-388(1998).
 CC -!- FUNCTION: Rubredoxin is a small nonheme, iron protein lacking
 CC acid-labile sulfide. Its single Fe, chelated to 4 Cys, functions
 CC as an electron acceptor and may also stabilize the conformation of
 CC the molecule (By similarity).
 CC -!- COFACTOR: Bands 1 iron(III) ion per subunit (By similarity).
 CC -!- SIMILARITY: Belongs to the rubredoxin family.
 CC -!- SIMILARITY: Contains 1 rubredoxin-like domain.

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EMBL; AE001266; AAC65947.1; -
PIR; G71256; G71256.
HSSP; P00268; LIRO.
TIGR; TP0991; -
InterPro; IPR004039; Rubredox.
InterPro; IPR001052; Rubredoxin.
Pfam; PF00301; Rubredoxin; 1.
PRINTS; PR00163; RUBREDOXIN.
ProDom; PD001610; Rubredox; 1.
PROSITE; PS00202; RUBREDOXIN; 1.
PROSITE; PSS09003; RUBREDOXIN_LIKE; 1.
Complete proteome; Electron transport; Iron; Metal-binding;
Rubredoxin.
DOMAIN 1 52 Rubredoxin-like.
FT

```

FT METAL      6      6      Iron (By similarity).
FT METAL      9      9      Iron (By similarity).
FT METAL     39     39      Iron (By similarity).
FT METAL     42     42      Iron (By similarity).
SQ SEQUENCE   52 AA;  5568 MW;  A76C9F012A70F1E1 CRC64;

Query Match      100.0%; Score 69; DB 1; Length 52;
Best Local Similarity 10.8%; Pred. No. 5.2e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

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RESULT 11	
Q6QAU0	PRELIMINARY; PRT; 52 AA.
ID	Q6QAU0
AC	O6QAU0;
DT	05-JUL-2004 (TREMBlrel. 27, Created)
DT	05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT	05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE	MST84DC.
GN	Names=Mst84DC; ORFNames=CG17945;
OS	Drosophila mauritiana (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Cephyroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7226;	
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=G52;
RA	Michael P., Noor M.A.F.;
RL	Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL: AV549556; AAS55565.1; -
DR	GO: GO:0005376; C:extracellular; IEA.
DR	GO: GO:0006952; P:defense response; IEA.
DR	GO: GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR	InterPro: IPR001450; 4FE4s ferredoxin.
DR	InterPro: IPR006081; Defensin_alpha.
DR	InterPro: IPR001007; VWF C.
DR	PROSITE: PS00199; 4FE4s_FERREDOXIN; UNKNOWN_2.
DR	PROSITE: PS00269; DEFENSIN; 1.
DR	PROSITE: PS01208; VWF C.1; UNKNOWN_1.
DR	SEQUENCE 52 AA: 4908 MW: DE0F3DE43F686E3A CRC64:
SO	

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Query Match      100.0%;   Score 69;   DB 2;   Length 52;
Best local Similarity 10.8%;   Pred. No. 5.2e+02;
Matches    4;   Conservative    33;   Mismatches    0;   Indels    0;   Gaps    0;

Qy      1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCCXC 37
        |||:|||||||:|||||||:|||||||:|:|
Db      3 CGPGSCCGCYCCGPCGGPCGCGPCGCCGCGCGPC 39

RESULT 12
Q9X709          PRELIMINARY;           PRT;       52 AA.
ID   Q9X709          AC   Q9X709;
DT   -01-NOV-1999   (TrEMBLrel. 12, Created)
DD   01-NOV-1999   (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003   (TrEMBLrel. 25, Last annotation update)
DE   Rubredoxin.
GN   Name=rub;
OS   Clostridium cellulolyticum.
OC   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1521;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 35319;
RA   Payot S., Gerard P., Petitdemange H.;
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
```

```

RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=ATCC 35319;
RA  Guedon E.;
RL  Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC  -1- SIMILARITY: Belongs to the rubredoxin family.
CC  -1- SIMILARITY: Contains 1 rubredoxin-like domain.
DR  EMBL; AJ238458; CAB41597.1; -
DR  HSSP; P00270; 1RDG.
DR  GO; GO:0005489; F:electron transporter activity; IEA.
DR  GO; GO:0046872; F:metal ion binding; IEA.
DR  GO; GO:0006118; P:electron transport; IEA.
DR  GO; GO:0006118; P:electron transport; IEA.
DR  InterPro; IPR004039; Rubredox.
DR  InterPro; IPR001052; Rubredoxin.
DR  Pfam; PF00301; Rubredoxin; 1.
DR  PRINTS; PR00163; RUBREDOXIN.
DR  ProDom; PD001610; Rubredox; 1.
DR  PROSITE; PS00202; RUBREDOXIN; 1.
DR  PROSITE; PS0903; RUBREDOXIN LIKE; 1.
KW  Electron transport; Iron; Metal-binding; Rubredoxin.
SQ  SEQUENCE 52 AA; 5658 MW; AF0F517D000E2FED CRC64;

Query Match 100.0%; Score 69; DB 2; Length 52;
Best Local Similarity 10.8%; Pred. No. 5.2e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

QY  1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 37
DB  6 CTVCVYDPEGDPGGIAPGTAFEDIPEDWVCPCLC 42

RESULT 13
ID  Q8R870 PRELIMINARY; PRT; 52 AA.
AC  Q8R870;
DT  01-JUN-2002 (TrEMBLrel. 21, Created)
DT  01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT  01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE  Rubredoxin.
GN  OrderedLocusNames=TTE2154;
OS  Thermoanaerobacter tengcongensis.
OC  Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC  Thermoanaerobacteriaceae; Thermoanaerobacter.
OX  NCBI_TaxID=119072;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=MB4;
RX  MEDLINE=21992816; PubMed=11997336; DOI=10.1101/gr.219302;
RA  Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA  Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA  Tan H., Chen R., Wang J., Yu J., Yang H.;
RT  "A complete sequence of the T. tengcongensis genome.";
RL  Genome Res. 12:689-700(2002)
CC  -1- SIMILARITY: Belongs to the rubredoxin family.
CC  -1- SIMILARITY: Contains 1 rubredoxin-like domain.
DR  EMBL; AE013163; AAM25316.1; -
DR  HSSP; P00270; 1RDG.
DR  GO; GO:0005489; F:electron transporter activity; IEA.
DR  GO; GO:0046872; F:metal ion binding; IEA.
DR  GO; GO:0006118; P:electron transport; IEA.
DR  InterPro; IPR004039; Rubredox.
DR  InterPro; IPR001052; Rubredoxin.
DR  PRINTS; PR00163; RUBREDOXIN.
DR  ProDom; PD001610; Rubredox; 1.
DR  PROSITE; PS00202; RUBREDOXIN; 1.
DR  PROSITE; PS0903; RUBREDOXIN LIKE; 1.
KW  Complete proteome; Electron transport; Iron; Metal-binding;
KW  Rubredoxin.
SQ  SEQUENCE 52 AA; 5825 MW; 1B01B1A08F621880 CRC64;

Query Match 100.0%; Score 69; DB 2; Length 52;
Best Local Similarity 10.8%; Pred. No. 5.2e+02;

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Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

QY  1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 37
DB  6 CTVCVYDPEKDPGSGQIPGTFPELPDWDWVCPDC 42

RESULT 14
ID  Q73NV0 PRELIMINARY; PRT; 52 AA.
AC  Q73NV0;
DT  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE  Rubredoxin.
GN  OrderedLocusNames=TDE1052;
OS  Treponema denticola.
OC  Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX  NCBI_TaxID=158;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=ATCC 35405 / DSM 14222;
RX  PubMed=15064399; DOI=10.1073/pnas.0307639101;
RA  Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
RA  Dodson R.J., Davidse T.M., DeBoy R.T., Fouts D.E., Haft D.H.,
RA  Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
RA  Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
RA  Gebregeorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B.,
RA  Shatsman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,
RA  Washist P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
RA  Weinstein G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
RT  "Comparison of the genome of the oral pathogen Treponema denticola
RT  with other spirochete genomes.";
RL  Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
CC  -1- SIMILARITY: Belongs to the rubredoxin family.
CC  -1- SIMILARITY: Contains 1 rubredoxin-like domain.
DR  EMBL; AE017249; AAS11541.1; -
DR  HSSP; P00268; 1B13.
DR  TIGR; TDE1052; -
DR  GO; GO:0005489; F:electron transporter activity; IEA.
DR  GO; GO:0046872; F:metal ion binding; IEA.
DR  GO; GO:0006118; P:electron transport; IEA.
DR  InterPro; IPR004039; Rubredox.
DR  InterPro; IPR001052; Rubredoxin.
DR  Pfam; PF00301; Rubredoxin; 1.
DR  PRINTS; PR00163; RUBREDOXIN.
DR  ProDom; PD001610; Rubredox; 1.
DR  PROSITE; PS00202; RUBREDOXIN; 1.
DR  PROSITE; PS0903; RUBREDOXIN LIKE; 1.
KW  Complete proteome; Electron transport; Iron; Metal-binding;
KW  Rubredoxin.
SQ  SEQUENCE 52 AA; 5544 MW; DC1D1D0723522AE CRC64;

Query Match 100.0%; Score 69; DB 2; Length 52;
Best Local Similarity 10.8%; Pred. No. 5.2e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

QY  1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 37
DB  6 CDLCGVYDPALGDPGGIAPGTAFEDIPDWDWVCPCLC 42

RESULT 15
ID  Q747S7 PRELIMINARY; PRT; 52 AA.
AC  Q747S7;
DT  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE  Rubredoxin.
GN  OrderedLocusNames=GSU3188;
OS  Geobacter sulfurreducens.
OC  Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;

```

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Query Match      100.0%; Score 69; DB 2; Length 52;
Best Local Similarity 10.8%; Pred. No. 5.2e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
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Search completed: May 27, 2005, 00:35:22
Job time : 176 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 00:30:06 ; Search time 495 Seconds
(without alignments)
87.306 Million cell updates/sec

Title: US-09-763-616-2

Perfect score: 69
Sequence: 1 CXKXXXXXXXCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_AA_Main:*

- 1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pcp.*
- 2: /cgn2_6/ptodata/1/paa/US06_COMB.pcp.*
- 3: /cgn2_6/ptodata/1/paa/US07_COMB.pcp.*
- 4: /cgn2_6/ptodata/1/paa/US08_COMB.pcp.*
- 5: /cgn2_6/ptodata/1/paa/US081_COMB.pcp.*
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- 14: /cgn2_6/ptodata/1/paa/US090_COMB.pcp.*
- 15: /cgn2_6/ptodata/1/paa/US091_COMB.pcp.*
- 16: /cgn2_6/ptodata/1/paa/US092_COMB.pcp.*
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- 19: /cgn2_6/ptodata/1/paa/US095_COMB.pcp.*
- 20: /cgn2_6/ptodata/1/paa/US096_COMB.pcp.*
- 21: /cgn2_6/ptodata/1/paa/US097A_COMB.pcp.*
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- 36: /cgn2_6/ptodata/1/paa/US110_COMB.pcp.*
- 37: /cgn2_6/ptodata/1/paa/US60_COMB.pcp.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	69	100.0	37	22	US-09-763-616-2	Sequence 294, Appl
3	69	100.0	37	29	US-10-351-334-294	Sequence 33, Appl
4	69	100.0	38	37	US-60-273-808-33	Sequence 33, Appl
5	69	100.0	38	37	US-60-278-983-33	Sequence 22, Appl
6	69	100.0	39	1	PCT-US04-15318-22	Sequence 40, Appl
7	69	100.0	39	4	US-08-011-396A-40	Sequence 40, Appl
8	69	100.0	39	6	US-08-209-204B-40	Sequence 40, Appl
9	69	100.0	39	6	US-08-209-204D-40	Sequence 40, Appl
10	69	100.0	39	6	US-08-209-204E-40	Sequence 40, Appl
11	69	100.0	39	8	US-08-461-097-40	Sequence 40, Appl
12	69	100.0	39	8	US-08-461-097A-40	Sequence 40, Appl
13	69	100.0	39	8	US-08-466-446-40	Sequence 40, Appl
14	69	100.0	39	8	US-08-467-459A-40	Sequence 40, Appl
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16	69	100.0	39	8	US-08-467-459A-40	Sequence 40, Appl
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18	69	100.0	39	8	US-08-467-470-40	Sequence 40, Appl
19	69	100.0	39	8	US-08-467-906-40	Sequence 40, Appl
20	69	100.0	39	8	US-08-468-731A-40	Sequence 40, Appl
21	69	100.0	39	8	US-08-468-731A-40	Sequence 40, Appl
22	69	100.0	39	8	US-08-469-526-40	Sequence 40, Appl
23	69	100.0	39	8	US-08-469-549-40	Sequence 40, Appl
24	69	100.0	39	8	US-08-469-549-40	Sequence 40, Appl
25	69	100.0	39	8	US-08-470-335-40	Sequence 40, Appl
26	69	100.0	39	8	US-08-470-335B-40	Sequence 40, Appl
27	69	100.0	39	8	US-08-471-148-40	Sequence 40, Appl
28	69	100.0	39	8	US-08-471-833-40	Sequence 40, Appl
29	69	100.0	39	8	US-08-471-833-40	Sequence 40, Appl
30	69	100.0	39	8	US-08-471-855-40	Sequence 40, Appl
31	69	100.0	39	8	US-08-472-008-40	Sequence 40, Appl
32	69	100.0	39	8	US-08-472-065-40	Sequence 40, Appl
33	69	100.0	39	9	US-08-535-200A-40	Sequence 40, Appl
34	69	100.0	39	9	US-08-535-200-40	Sequence 40, Appl
35	69	100.0	39	11	US-08-734-592-40	Sequence 40, Appl
36	69	100.0	39	11	US-08-734-665-40	Sequence 40, Appl
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44	69	100.0	39	11	US-08-736-070A-40	Sequence 40, Appl
45	69	100.0	39	11	US-08-736-070-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
PCT-US99-17130-287
; Sequence 287, Application PC/TUS9917130
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031.PCT
; CURRENT APPLICATION NUMBER: PCT/US99/17130
; CURRENT FILING DATE: 1999-07-29
; EARLIER FILING DATE: 1998-07-30
; EARLIER FILING DATE: 1998-07-30
; EARLIER FILING DATE: 1998-07-30
; EARLIER FILING DATE: 1998-08-05
; EARLIER FILING DATE: 1998-08-05
; EARLIER FILING DATE: 1998-08-06
; EARLIER FILING DATE: 1998-08-06
; EARLIER FILING DATE: 1998-08-06
; EARLIER FILING DATE: 1998-08-12

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 287
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-17130-287

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Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-763-616-2
; Sequence 2, Application US/09763616
; GENERAL INFORMATION:
; APPLICANT: BERNARD, HANS-ULRICH
; APPLICANT: TAN, YEE JOO
; APPLICANT: BEERHEIDE, WALTER
; APPLICANT: TING, ANTHONY EUGENE
; APPLICANT: SIM, MUI MUI
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS AND METHODS
; FILE REFERENCE: BERN3001/JDB
; CURRENT APPLICATION NUMBER: US/09/763,616
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: PCT/AU99/00724
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: AU PQ1645/99
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: AU PP5733/98
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
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; LOCATION: (2)..(3)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(33)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (35)..(36)
; OTHER INFORMATION: Variable amino acid
; OTHER INFORMATION: Variable amino acid
US-09-763-616-2

Query Match      100.0%; Score 69; DB 22; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37

RESULT 3
US-10-351-334-294
; Sequence 294, Application US/10351334
; GENERAL INFORMATION:
; APPLICANT: Komatsoulis et al
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; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P2
; CURRENT APPLICATION NUMBER: US/10/351,334
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/350,898
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/489,847
; PRIOR FILING DATE: 2000-01-24
; PRIOR APPLICATION NUMBER: PCT/US99/17130
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 60/094,657
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: 60/095,486
; PRIOR FILING DATE: 1998-08-05
; PRIOR APPLICATION NUMBER: 60/096,319
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: 60/095,454
; PRIOR FILING DATE: 1998-08-06
; PRIOR APPLICATION NUMBER: 60/095,455
; PRIOR FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 294
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-351-334-294

Query Match      100.0%; Score 69; DB 29; Length 37;
Best Local Similarity 10.8%; Pred. No. 3.2e+03;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-60-273-808-33
; Sequence 33, Application US/60273808
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: D0134
; CURRENT APPLICATION NUMBER: US/60/273,808
; CURRENT FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 38
; TYPE: PRT
; ORGANISM: homo sapiens
US-60-273-808-33

Query Match      100.0%; Score 69; DB 37; Length 38;
Best Local Similarity 10.8%; Pred. No. 3.2e+03;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

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Db 2 CAGCAGCGCGCGCATGTACACGCGGTCTGCTGCTGCCGC 38

RESULT 5
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; Sequence 33, Application US/60278983
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: D0134.ppt
; CURRENT APPLICATION NUMBER: US/60/278,983
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; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,204
; FILING DATE: 08-MAR-1994
; APPLICATION DATA:
; APPLICATION NUMBER: 08/059,022
; FILING DATE: 06-MAY-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04585/028001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: 200154
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
US-08-461-097-40

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Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

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Db 3 CGCKCRTCACRCAGAGGTCTTCTCTTCAGC 39

RESULT 13
US-08-461-097A-40
; Sequence 40, Application US/08461097A
; GENERAL INFORMATION:
; APPLICANT: Sklar, Robert
; APPLICANT: Marchionni, Mark
; APPLICANT: Gwynne, David
; TITLE OF INVENTION: METHODS FOR TREATING MUSCLE
; TITLE OF INVENTION: DISEASES AND DISORDERS
; NUMBER OF SEQUENCES: 383
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,097A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/059,022
; FILING DATE: 06-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,204
; FILING DATE: 08-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bleker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
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; REFERENCE/DOCKET NUMBER: 04585/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-461-097A-40

Query Match 100.0%; Score 69; DB 8; Length 39;
Best Local Similarity 10.8%; Pred. No. 3.4e+03;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXC 37
Db 3 CGCKCRTCACRCAGAGGTCTTCTCTTCAGC 39

RESULT 14
US-08-466-446-40
; Sequence 40, Application US/08466446
; GENERAL INFORMATION:
; APPLICANT: Gwynne, David I.; Marchionni, Mark;
; APPLICANT: McBurney, Robert N.
; TITLE OF INVENTION: INHIBITORS OF CELL PROLIFERATION,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; ZIP: 0211-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,446
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/011,396
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/984,085
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/951,747
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/927,337
; FILING DATE: 10-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04585/017004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: 200154
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
US-08-466-446-40
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OM protein - protein search, using sw model

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(without alignments)
81.197 Million cell updates/sec

Title: US-09-763-616-2

Perfect score: 69
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Searched: 537409 seqs, 114114291 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep.*
- 8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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6	69	100.0	63	7	US-11-097-143-26472
7	69	100.0	66	8	US-60-669-241-25327
8	69	100.0	71	7	US-11-079-463-9113
9	69	100.0	71	7	US-11-079-045-9113
10	69	100.0	72	7	US-11-097-143-26460
11	69	100.0	74	7	US-11-097-143-26457
12	69	100.0	76	6	US-10-703-032-107111
13	69	100.0	76	6	US-10-703-032-192031
14	69	100.0	80	8	US-60-669-175-32704
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19	69	100.0	92	6	US-10-703-032-164331
20	69	100.0	92	8	US-60-655-875-123185
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22	69	100.0	93	6	US-10-703-032-159412
23	69	100.0	93	6	US-10-703-032-192934
24	69	100.0	95	6	US-10-703-032-105601
25	69	100.0	97	6	US-10-530-253-29

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Sequence 3, Appli
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Sequence 168355,
Sequence 170437,
Sequence 5, Appli
Sequence 65, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 65, Appli
Sequence 30, Appli
Sequence 34, Appli
Sequence 106880,
Sequence 16481, A

US-10-526-324-813
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PCT-US04-13756-3
PCT-US04-05292A-6
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US-10-530-253-28
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US-10-703-032-106880
US-11-031-175-16481

ALIGNMENTS

RESULT 1

US-10-526-324-813
; Sequence 813, Application US/10526324
; GENERAL INFORMATION:
; APPLICANT: Imanaka, Takayuki
; TITLE OF INVENTION: METHOD OF TARGETED GENE DISRUPTION, GENOME OF
; TITLE OF INVENTION: HYPERTHERMOSTABLE BACTERIUM AND GENOME CHIP USING
; TITLE OF INVENTION: THE SAME
; FILE REFERENCE: 490051.401USPC
; CURRENT APPLICATION NUMBER: US/10/526,324
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: PCT/IB2003/003597
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: JP 2002-319011
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 2167
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 813
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Thermococcus kodakaraensis KOD1
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (414542)..(414542)
; OTHER INFORMATION: n is a o r c o r g o r t.
; FEATURE:
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; LOCATION: (786890)..(786890)
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; NAME/KEY: misc_feature


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Query Match      100.0%; Score 69; DB 7; Length 63;
Best Local Similarity 10.8%; Pred. No. 1.5e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
Db 26 CGGCGPCGGCGPCGCGCGCGCGTSSFCGCGPC 62

RESULT 7
US-60-669-241-25327
; Sequence 25327, Application US/60669241
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; APPLICANT: Baum, James A
; APPLICANT: Gilbertson, Larry A
; APPLICANT: Kovalic, David K
; APPLICANT: Lakosa, Thomas J
; APPLICANT: Lu, Maolong
; APPLICANT: Munyikwa, Tichifa R. I.
; APPLICANT: Roberts, James K
; APPLICANT: Wu, Wei
; APPLICANT: Zhang, Bei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CONTROL OF INSECT INFESTATION IN PLA
; FILE REFERENCE: 38-21(53596)
; CURRENT APPLICATION NUMBER: US/60/669,241
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60560842
; PRIOR FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60565632
; PRIOR FILING DATE: 2004-04-27
; PRIOR APPLICATION NUMBER: 60579062
; PRIOR FILING DATE: 2004-06-11
; PRIOR APPLICATION NUMBER: 60603421
; PRIOR FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: 60617261
; PRIOR FILING DATE: 2004-10-11
; NUMBER OF SEQ ID NOS: 50011
; SEQ ID NO 25327
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Lygus hesperus
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna-SeqID_411; Strand=-; Position=985-
US-60-669-241-25327

Query Match      100.0%; Score 69; DB 8; Length 66;
Best Local Similarity 10.8%; Pred. No. 1.6e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
Db 10 CASCTNCTNSFNLSCLDKCKRYRTSCSCTGTCTNC 46

RESULT 8
US-11-079-463-9113
; Sequence 9113, Application US/11079463
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 9113

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; LENGTH: 71
; TYPE: PRT
; ORGANISM: B.fragilis
US-11-079-463-9113

Query Match      100.0%; Score 69; DB 7; Length 71;
Best Local Similarity 10.8%; Pred. No. 1.8e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
Db 23 CTVCDFIYDPEIGDPEGIEPGTGFEDIPDDWVCPLC 59

RESULT 9
US-11-079-045-9113
; Sequence 9113, Application US/11079045
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR
; FILE REFERENCE: PATH00-03DIV1
; CURRENT APPLICATION NUMBER: US/11/079,045
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 9113
; LENGTH: 71
; TYPE: PRT
; ORGANISM: B.fragilis
US-11-079-045-9113

Query Match      100.0%; Score 69; DB 7; Length 71;
Best Local Similarity 10.8%; Pred. No. 1.8e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
Db 23 CTVCDFIYDPEIGDPEGIEPGTGFEDIPDDWVCPLC 59

RESULT 10
US-11-097-143-26460
; Sequence 26460, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26460
; LENGTH: 72
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-26460

Query Match      100.0%; Score 69; DB 7; Length 72;
Best Local Similarity 10.8%; Pred. No. 1.8e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXC 37
Db 17 CGPCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 53

RESULT 11
US-11-097-143-26457
; Sequence 26457, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26457
; LENGTH: 74
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-26457

Query Match      100.0%; Score 69; DB 7; Length 74;
Best Local Similarity 10.8%; Pred. No. 1.9e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXC 37
Db 9 CGPCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 45

RESULT 12
US-10-703-032-107111
; Sequence 107111, Application US/10703032
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Andersen, Scott E.
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Cao, Yongwei
; APPLICANT: Masucci, James D.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With

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; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53374)B
; CURRENT APPLICATION NUMBER: US/10/703,032
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: 10/020,338
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 211164
; SEQ ID NO 107111
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_TA_1529.pep
US-10-703-032-107111

Query Match      100.0%; Score 69; DB 6; Length 76;
Best Local Similarity 10.8%; Pred. No. 2e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXC 37
Db 31 CPSCGGPVATDVESERRILCLPLCLKSKKYYCTRC 67

RESULT 13
US-10-703-032-192031
; Sequence 192031, Application US/10703032
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Andersen, Scott E.
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Cao, Yongwei
; APPLICANT: Masucci, James D.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(53374)B
; CURRENT APPLICATION NUMBER: US/10/703,032
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: 10/020,338
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 211164
; SEQ ID NO 192031
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(76)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_TA_86449.pep
US-10-703-032-192031

Query Match      100.0%; Score 69; DB 6; Length 76;
Best Local Similarity 13.5%; Pred. No. 2e+02;
Matches 5; Conservative 32; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXC 37
Db 14 CKNCCACCCGCGCGCGCGCGCGCGCGCGCGCGC 50

RESULT 14
US-60-669-175-32704
; Sequence 32704, Application US/60669175
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; APPLICANT: Baum, James A.
; APPLICANT: Gilbertson, Larry A.
; APPLICANT: Kovalic, David K.
; APPLICANT: LaRosa, Thomas J

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Fri May 27 09:41:02 2005

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; APPLICANT: Lu, Maolong
; APPLICANT: Munyikwa, Tichifa R. I.
; APPLICANT: Roberts, James K
; APPLICANT: Wu, Wei
; APPLICANT: Zhang, Bei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CONTROL OF INSECT INFESTATION IN PLA
; FILE REFERENCE: 38-21(53597)
; CURRENT APPLICATION NUMBER: US/60/669,175
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60560842
; PRIOR FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60565632
; PRIOR FILING DATE: 2004-04-27
; PRIOR APPLICATION NUMBER: 60579062
; PRIOR FILING DATE: 2004-06-11
; PRIOR APPLICATION NUMBER: 60603421
; PRIOR FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: 60617261
; PRIOR FILING DATE: 2004-10-11
; NUMBER OF SEQ ID NOS: 40774
; SEQ ID NO 32704
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Diabrotica virgifera
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID_12401; Strand=-; Position=59
US-60-669-175-32704
```

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Query Match      100.0%; Score 69; DB 8; Length 80;
Best Local Similarity 10.8%; Pred. No. 2.1e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
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Qy      1  CXCXXXXXXX
Db      21  CVVCAKSLQYTKLYNPSYVEWIIINLLFLSGVCRGC 57
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RESULT 15
US-10-467-657-5372
; Sequence 5372, Application US/10467657
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5372
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5372
```

```

Query Match      100.0%; Score 69; DB 6; Length 84;
Best Local Similarity 10.8%; Pred. No. 2.3e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
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```

Qy      1  CXCXXXXXXX
Db      34  CGPCGWYDELGDEHGIAFGTKFEDIPDDWKCEFC 70
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Search completed: May 27, 2005, 00:46:14
Job time : 53 secs